	ACCATGCACTCGCTGGGCTTCTTCTGTGGCGTGTTCTCTGCTGCCGCTG	.09
-	CAGGAAGGTGGTACGTGAGCACCGAAGAAGAGACACCGCACAAGAGACGACGGCGACAACA	1
61	CGCTGCTCCCGGGTCCTCGCGAGGCGCCCCCCCCCCCCC	120
21	ACCTCTCGGACGCGGACGCGGGGGGGCCACGGCTTATGCAAGCAA	180
81	AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT ++++++	240
ر د	ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAACAGG	300
_ੀ ਹਾਂ	TAACCITITACATGTTCACAGTCGATTCCTTTCCTCCGACCGTTGTATTGTCTTTGTCC W K M Y K C Q L R K G G W Q H N R E Q A	i
	CCAACCTCAACTCAAGGACAGAGAGAGTTTAAAATTTGCTGCAGCACATTATAATACAG	
	MATCH WITH FIG. 1B Fig. 1A	_

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	MATCH WITH FIG. 1A++++++++-	360
AGAT 361	AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGC	20
TCT	TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACG	
GTA CAT	GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG++++++++-	480
TGJ ACA	TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCAAAAAAAA	540
S		- 009
CGT	CGTGCTCGATGGAGTCGTTCTGCAATAACTTTAATGTCACGGAGAGAGA	
AAC	AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG	099
TTC		
	MATCH WITH FIG. 1C Fig. 1B	

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	MANDH WITH BIG 1B	
Š	TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCAGAGTGTC	720
661	AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAGAG	
721	AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCCCCACCATGTGCAGATGCCCAGATGCCCAGATGCCCAGATGCCCAGATGCAGATGCAGATGCAGATGCAGATGTGTGTG	780
		1 0
781	ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGGAGCCTACGACCTCTACTAGGTTGTCTACCTAAGGAGCCTACGACCTCTACTAGGTTGTCTACCTAAGG) * 0 i
•	ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGAGACCTGTCAGTGTGTCTGCAGAG	006
841	TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACAGACGTCTC D I C G P N K E L D E E T C Q C V C R A	ı
Ċ	CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAGAACTAGACAGAAACTCATGCCAGT	096
9 U L	GCCCCGAAGCCGGACGTCTGGGGTGTTTCTTGATCTGTTTGAGTACGGTCACGGTCACCCCGAAGCCGGACGGTCGTCTTCTTGATCTTGAGTACGGTCAC	t
190	GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCCAACCGAGAATTTGATGAAA	1020
T O C	CACAGACATTTTTGTTTGAGAGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT MATCH WITH FIG. 1D	

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MATCH WITH FIG. 1E

Fig. 1D

261	MATCH WITH FIG. 1D++++++ TTTACTCGATTCTAACATGACAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA	1320
321	TGCCA 	1380
381	AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG	1440
441	CAAAAGGCCTCTTGTAAAGAETGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC 	1500
501	TTGTGATTTCTTTAAAAGAATGACTATATAAATTTATTTCCACTAAAAATATTCTGC 	1560
561	ATTCATTTTTATAGCAACAACTGGTAAAACTCACTGTGATCAATATTTTTATATCAT 	1620
621	GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAA	

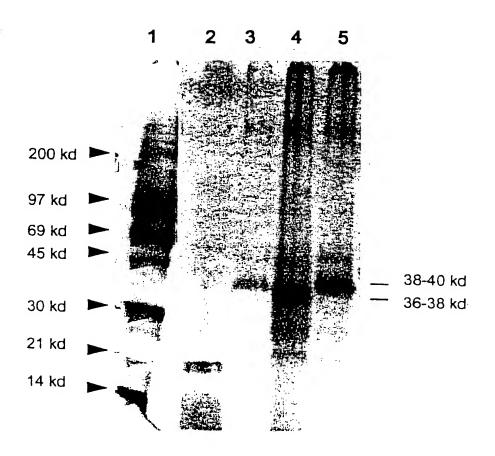
Fig. 1E

N A H E	04	0.05-5-5	
LORLL LORLL AKWSO SGWQH	100 EEAVP AEPAMI	25 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	200 ARPVT EKKSV VHSII
SIRDLORLLE SFDDLORLLH LHHAKWSOA LRKGGWOHN	SLTI.	NTSS/ NNRN/ NDEGL NSEGL	AT ETVAA DRARQ DVYRQ
RSQ1H OHS1R	.RSI.	7600 SGCC SGCC SGCC	SPKK N
1 Pdgfo MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSOIH SIRDLORLLE Pdgfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLORLLH VegfMNFLL SWVHWSLALL LYLHHAKWSQA	Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSIEEAVP Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES LARGRRSLG SLTIAEPAMI Vegf APMAEGGGQ NHHEVVKFMD .VYQR	SANFLIMPPC VEVKRCTGCC NTSSVKGOPS NANFLVMPPC VEVQRCSGCC NNRNVQCRPTEYIFKPSC VPLMRCGGCC NDEGLEGVPTNTFFKPPC VSVYRCGGCC NSEGLOCMNT	Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLEGAG AT Pdgfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKG ETVAAARPVT Vegf EESNITMOIM RIK.PH CC QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
PREV PEEL	EKRP I S KFMD KSID N	APPC V SPC V SPC V SPC V	CEE H
KEEAE I KEGOP I Y	TKHVP GGELE HHEVVI NTEILI	ANFL IV ANFL VV EY I FY	(EVQVF (KATVI HIGEMS (PVTIS
VL	A N N N	S N · ·	メニ 0 0 ユ ⊊ 早 実
rLAH' rLRL' VSLAI WKM`	AHGV MTRS . GGC	QVDP L I DR YPDE FGVA	KKKP KKKP 1 Q
LGCG) SLCC) SWVHW	OTSLR ELDLN 	Pdgfa AVCKTRTVIY EIPRSQVDPT Pdgfb AECKTRTEVF EISRRLIDRT Vegf SYCHPIETLV DIFQEYPDEI Vegf2 TQCMPREVCI DVGKEFGVAT	(VEYV)
1 .MRTLACLLL MNRCWA.LFL MNFLL	DSL DGA 	VIY	VA K VR K VIM R
TLAC CWA.	VGSE GEE AE	(TRT) (TRTE IPIE ⁻ IPRE)	RSVK RPVC ITMC LSKT
MNR	51 IDS' CDP APM	1 S R S O O O O O O O O O O O O O O O O O	151 RVHH QVQL EESN STSY
1 Pdgfa .MRTLACLLL Pdgfb MNRCWA.LFL VegfMNFLL	dgfa dgfb Vegf egf2	101 Pdgfa AVCKTRTVIY Pdgfb AECKTRTEVF Vegf SYCHPIETLV Vegf2 TQCMPREVCI	lgfa Igfb (egf 1 gf2
ии >	<u> </u>	9,9,2,3,	2

Fig. 2A

250 DKTALKETLG SLPGPHP	300 QTCKCSCKNT NSCQCVCKNK	350 CTESPQKCLL	398 YWQRPQMS
GKHRKFKHTH VGARCCLMPW CLAQEDFMFS	RRKHLFVQDP PHKEL DR	350 DSRCKARQ LELNERTCRC DKPRR. LFPSQCGANR EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL	351 Pdgfa
RTVRVRRPPK KSRYKSWSVY NYMMNNHICR	LDEETCQCVC RAGLRPASCG	DKPRR	OKACEPGFSY
YREEDTDVR. AKTPQTRVTI .GKGQKRKRK CQAANKTCPT	LDEETCOCVC	LELNERTCRC EFDENTCQC	351
201 TSLNPD RSPGGSQEQR / RGK	251 Pdgfa Pdgfb A		351 KGKKFHHQTC
Pdgfa Pdgfb Vegf Vegf	Pdgfa Pdgfb Vegf Vegf	Pdgfa Pagfb Vegf Vegf2	Pdgfa Pdgfb Vegf Vegf2

Fig. 2B

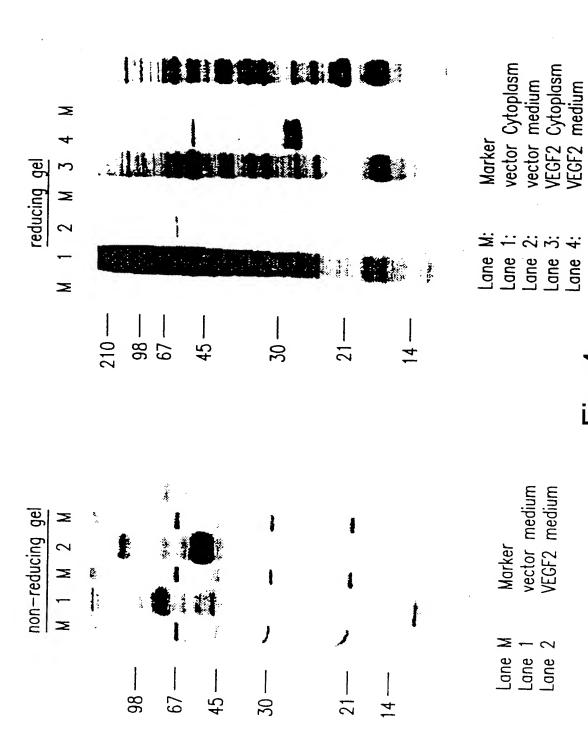


Lane 1: 14-C and rainbow M.W. marker

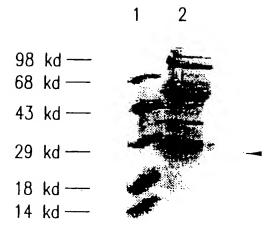
Lane 2: FGF control

Lane 3: VEGF2 (M13-reverse \$ forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

Fig. 3



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Lane 1: Lane 2: Molelular weight marker Precipitates containing VEGF2.

Fig. 5

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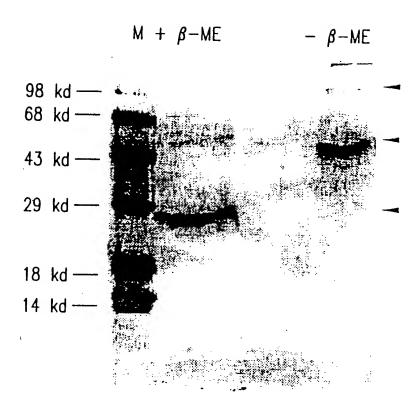


Fig. 6

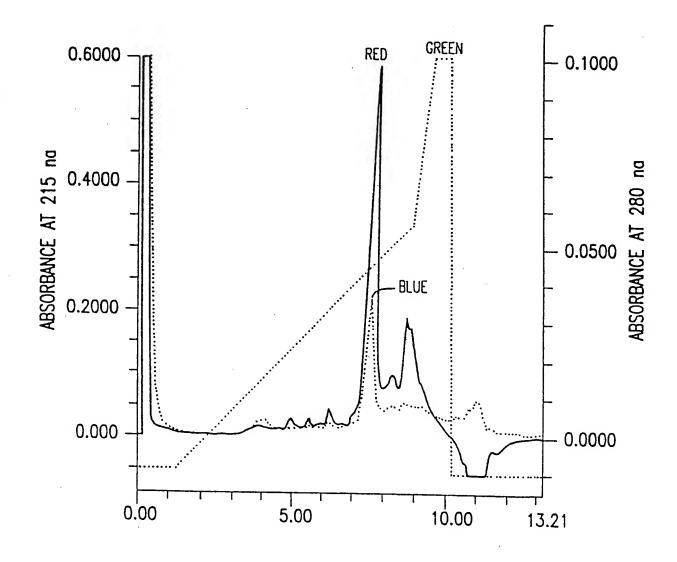


Fig. 7

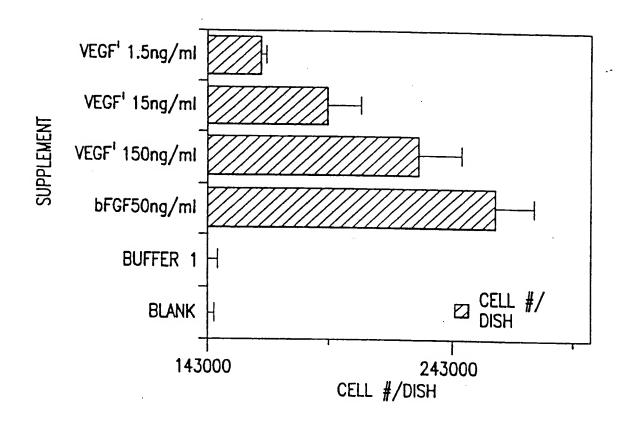


Fig. 8

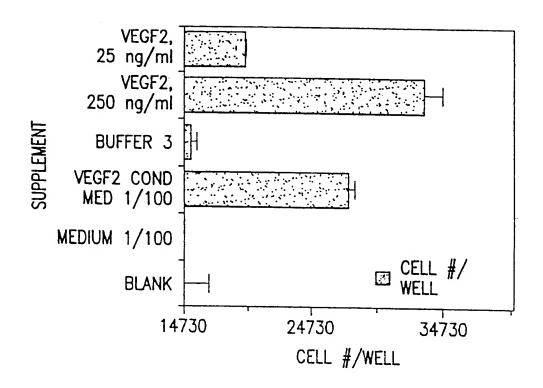


Fig. 9